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CONTENTS/SUMMARIES

Summary: Cyclic β-glucans are low-molecular-weight cell surface carbohydrates that are found almost exclusively in bacteria of the Rhizobiaceae family. These glucans are major cellular constituents, and under certain culture conditions their levels may reach up to 20% of the total cellular dry weight. In Agrobacterium and Rhizobium species, these molecules contain between 17 and 40 glucose residues linked solely by β-(1,2) glycosidic bonds. In Bradyrhizobium species, the cyclic β-glucans are smaller (10 to 13 glucose residues) and contain glucose linked by both β-(1,6) and β-(1,3) glycosidic bonds. In some rhizobial strains, the cyclic β-glucans are unsubstituted, whereas in other rhizobia these molecules may become highly substituted with moieties such as sn-1-phosphoglycerol. To date, two genetic loci specifically associated with cyclic β-glucan biosynthesis have been identified in Rhizobium (ndvA and ndvB) and Agrobacterium (chvA and chvB) species. Mutants with mutations at these loci have been shown to be impaired in their ability to grow in hypoosmotic media, have numerous alterations in their cell surface properties, and are also impaired in their ability to infect plants. The present review will examine the structure and occurrence of the cyclic β-glucans in a variety of species of the Rhizobiaceae. The possible functions of these unique molecules in the free-living bacteria as well as during plant infection will be discussed.

Summary: Bacterial conjugation results in the transfer of DNA of either plasmid or chromosomal origin between microorganisms. Transfer begins at a defined point in the DNA sequence, usually called the origin of transfer (oriT). The capacity of conjugative DNA transfer is a property of self-transmissible plasmids and conjugative transposons, which will mobilize other plasmids and DNA sequences that include a compatible oriT locus. This review will concentrate on the genes required for bacterial conjugation that are encoded within the transfer region (or regions) of conjugative plasmids. One of the best-defined conjugation systems is that of the F plasmid, which has been the paradigm for conjugation systems since it was discovered nearly 50 years ago. The F transfer region (over 33 kb) contains about 40 genes, arranged contiguously. These are involved in the synthesis of pili, extracellular filaments which establish contact between donor and recipient cells; mating-pair stabilization; prevention of mating between similar donor cells in a process termed surface exclusion; DNA nicking and transfer during conjugation; and the regulation of expression of these functions. This review is a compendium of the products and other features found in the F transfer region as well as a discussion of their role in conjugation. While the genetics of F transfer have been described extensively, the mechanism of conjugation has proved elusive, in large part because of the low levels of

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expression of the pilus and the numerous envelope components essential for F plasmid transfer. The advent of molecular genetic techniques has, however, resulted in considerable recent progress. This summary of the known properties of the F transfer region is provided in the hope that it will form a useful basis for future comparison with other conjugation systems.

Summary: This review compares the results of different methods of investigating the morphology of nucleoids of bacteria grown under conditions favoring short generation times. We consider the evidence from fixed and stained specimens, from phase-contrast and fluorescence microscopy of growing bacteria, and from electron microscopy of whole as well as thinly sectioned ones. It is concluded that the nucleoid of growing cells is in a dynamic state: part of the chromatin is "pulled out" of the bulk of the nucleoid in order to be transcribed. This activity is performed by excrescences which extend far into the cytoplasm so as to reach the maximum of available ribosomes. Different means of fixation provide markedly different views of the texture of the DNA-containing plasm of the bulk of the nucleoid. Conventional chemical fixatives stabilize the cytoplasm of bacteria but not their protein-low chromatin. Uranyl acetate does cross-link the latter well but only if the cytoplasm has first been fixed conventionally. In the interval between the two fixations, the DNA arranges itself in liquid-crystalline form, supposedly because of loss of supercoiling. In stark contrast, cryofixation preserves bacterial chromatin in a finely granular form, believed to reflect its native strongly negatively supercoiled state. In dinoflagellates the DNA of their permanently visible chromosomes (also low in histone-like protein) is natively present as a liquid crystal. The arrangement of chromatin in Epulocystis fishelsoni, one of the largest known prokaryotes, is briefly described.

Summary: Ciliates contain two types of nuclei: a micronucleus and a macronucleus. The micronucleus serves as the germ line nucleus but does not express its genes. The macronucleus provides the nuclear RNA for vegetative growth. Mating cells exchange haploid micronuclei, and a new macronucleus develops from a new diploid micronucleus. The old macronucleus is destroyed. This conversion consists of amplification, elimination, fragmentation, and splicing of DNA sequences on a massive scale. Fragmentation produces subchromosomal molecules in Tetrahymena and Paramecium cells and much smaller, gene-sized molecules in hypotrichous ciliates to which telomere sequences are added. These molecules are then amplified, some to higher copy numbers than others. rDNA is differentially amplified to thousands of copies per macronucleus. Eliminated sequences include transposonlike elements and sequences called internal eliminated sequences that interrupt gene coding regions in the micronuclear genome. Some, perhaps all, of these are excised as circular molecules and destroyed. In at least some hypotrichs, segments of some micronuclear genes are scrambled in a nonfunctional order and are reordered during macronuclear development. Vegetatively growing ciliates appear to possess a mechanism for adjusting copy numbers of individual genes, which corrects gene imbalances resulting from random distribution of DNA molecules during amitosis of the macronucleus. Other distinctive features of ciliate DNA include an altered use of the conventional stop codons.

Summary: The early notion of DNA as a passive target for regulatory proteins has given way to the realization that higher-order DNA structures and DNA-protein complexes are at the basis of many molecular processes, including control of promoter activity. Protein binding may direct the bending of an otherwise linear DNA, exacerbate the angle of an intrinsic bend, or assist the directional flexibility of certain sequences within prokaryotic promoters. The important, sometimes essential role of intrinsic or protein-induced DNA bending in transcriptional regulation has become evident in virtually every system examined. As discussed throughout this article, not every function of DNA bends is understood, but their presence has been detected in a wide variety of bacterial promoters subjected to positive or negative control. Nonlinear DNA structures facilitate and even determine proximal and distal DNA-protein and protein-protein contacts involved in the various steps leading to transcription initiation.